

#14



1600

RAW SEQUENCE LISTING

DATE: 06/14/2002

PATENT APPLICATION: US/09/471,459A

TIME: 14:50:24

Input Set : A:\PC10315A Sequence Listing.ST25.txt

Output Set: N:\CRF3\06142002\I471459A.raw

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3 <110> APPLICANT: Pfizer Inc.
 4 Fidock, Mark David
 6 <120> TITLE OF INVENTION: Enzyme PDE xiv
 8 <130> FILE REFERENCE: PC10315AGPR
 10 <140> CURRENT APPLICATION NUMBER: 09/471,459A
 11 <141> CURRENT FILING DATE: 1999-12-22
 13 <150> PRIOR APPLICATION NUMBER: GB 9828603.2
 14 <151> PRIOR FILING DATE: 1998-12-23
 16 <150> PRIOR APPLICATION NUMBER: GB 9922123.6
 17 <151> PRIOR FILING DATE: 1999-09-17
 19 <160> NUMBER OF SEQ ID NOS: 26
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 446
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Mouse
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 35 20 25 30
 38 Arg Gly Gln Thr Gly Val Pro Ala Glu Arg Arg Gly Ser Tyr Pro Phe
 39 35 40 45
 42 Ile Asp Phe Arg Leu Leu Asn Asn Thr Thr His Ser Gly Glu Ile Gly
 43 50 55 60
 46 Thr Lys Lys Lys Val Lys Arg Leu Leu Ser Phe Gln Arg Tyr Phe His
 47 65 70 75 80
 50 Ala Ser Arg Leu Leu Arg Gly Ile Ile Pro Gln Ala Pro Leu His Leu
 51 85 90 95
 54 Leu Asp Glu Asp Tyr Leu Gly Gln Ala Arg His Met Leu Ser Lys Val
 55 100 105 110
 58 Gly Thr Trp Asp Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly
 59 115 120 125
 62 Asn Ser Leu Val Thr Leu Leu Cys His Leu Phe Asn Ser His Gly Leu
 63 130 135 140
 66 Ile His His Phe Lys Leu Asp Met Val Thr Leu His Arg Phe Leu Val
 67 145 150 155 160
 70 Met Val Gln Glu Asp Tyr His Gly His Asn Pro Tyr His Asn Ala Val
 71 165 170 175
 74 His Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr Leu Lys Glu Pro
 75 180 185 190
 78 Lys Leu Ala Ser Phe Leu Thr Pro Leu Asp Ile Met Leu Gly Leu Leu
 79 195 200 205

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83      210      215      220
86 Leu Ile Lys Thr Asn His His Leu Ala Asn Leu Tyr Gln Asn Met Ser
87 225      230      235      240
90 Val Leu Glu Asn His His Trp Arg Ser Thr Ile Gly Met Leu Arg Glu
91      245      250      255
94 Ser Arg Leu Leu Ala His Leu Pro Lys Glu Met Thr Gln Asp Ile Glu
95      260      265      270
98 Gln Gln Leu Gly Ser Leu Ile Leu Ala Thr Asp Ile Asn Arg Gln Asn
99      275      280      285
102 Glu Phe Leu Thr Arg Leu Lys Ala His Leu His Asn Lys Asp Leu Arg
103      290      295      300
106 Leu Glu Asn Val Gln Asp Arg His Phe Met Leu Gln Ile Ala Leu Lys
107 305      310      315      320
110 Cys Ala Asp Ile Cys Asn Pro Cys Arg Ile Trp Glu Met Ser Lys Gln
111      325      330      335
114 Trp Ser Glu Arg Val Cys Glu Glu Phe Tyr Arg Gln Gly Asp Leu Glu
115      340      345      350
118 Gln Lys Phe Glu Leu Glu Ile Ser Pro Leu Cys Asn Gln Gln Lys Asp
119      355      360      365
122 Ser Ile Pro Ser Ile Gln Ile Gly Phe Met Thr Tyr Ile Val Glu Pro
123      370      375      380
126 Leu Phe Arg Glu Trp Ala Arg Phe Thr Gly Asn Ser Thr Leu Ser Glu
127 385      390      395      400
130 Asn Met Leu Ser His Leu Ala His Asn Lys Ala Gln Trp Lys Ser Leu
131      405      410      415
134 Leu Ser Asn Gln His Arg Arg Arg Gly Ser Gly Gln Asp Leu Ala Gly
135      420      425      430
138 Pro Ala Pro Glu Thr Leu Glu Gln Thr Glu Gly Ala Thr Pro
139      435      440      445

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142 <210> SEQ ID NO: 2

143 <211> LENGTH: 1341

144 <212> TYPE: DNA

145 <213> ORGANISM: Mouse

147 <400> SEQUENCE: 2

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152 gaacgccgtg gctcctaccc attcattgac ttccgtctac ttaacaatac aacacactca      180
154 ggggaaattg gcaccaagaa aaaggtgaaa cgactgttaa gtttccaaag atacttccat      240
156 gcatctaggc ttctccgggg gattataccg caggcccttc tccacctgct ggatgaagac      300
158 taccttggac aagcaaggca catgctctcc aaagttggaa cgtgggactt tgacattttc      360
160 ttgtttgatc gcttgacaaa tgggaacagt ctggttaactc tgttgtgtca cctcttcaac      420
162 tcccatgggc tcatccacca ttcaagctc gatatggtga ccttgcacag gtttctggtt      480
164 atggttcagg aagattacca cgtcacaac ccataccaca atgctgttca cgcagccgac      540
166 gtcacccagg ccatgcactg ttacctgaag gagccaaagt tggcaagctt cctcacacct      600
168 ctggacatca tggttggact actggctgca gcagctcatg acgtggacca cccaggggtc      660
170 aaccagccat ttttgatcaa aactaaccac catcttgcca acctgtatca gaatatgtct      720
172 gtactggaga atcaccactg gcgatctaca attggcatgc ttcgagaatc acggctcctg      780
174 gctcacttgc caaaggaaat gacacaggat atcgaacagc agctgggctc cctcatcttg      840

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178 aaagatttga gactggagaa tgtacaggac agacacttta tgcttcagat cgccttgaag 960
180 tgtgctgaca ttgcaatcc ttgtcgtatc tgggagatga gcaagcagtg gagtgaagag 1020
182 gtctgtgagg aattctacag acaagggtgac cttgaacaga agtttgaact ggaaatcagt 1080
184 cctcttttga atcaacagaa agattcaatc cctagcatac aaattggttt catgacttac 1140
186 atcgtggagc cgctgttccg ggagtgggccc cggtttactg ggaacagcac cctgtcggag 1200
188 aacatgctaa gccatctcgc gcacaacaaa gcccagtgga agagcctgct gtccaatcag 1260
190 cacagacgca ggggcagcgg ccaggacctg gcgggccccg cacctgagac cctggagcag 1320
192 acagaaggtg ccacgcccta a 1341
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196 <211> LENGTH: 288
197 <212> TYPE: PRT
198 <213> ORGANISM: Human
200 <400> SEQUENCE: 3
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203 1 5 10 15
206 Pro Asp Gln Asn Ala Lys Cys Val Cys Met Leu Gly Asp Ile Arg Leu
207 20 25 30
210 Arg Gly Gln Thr Gly Val Arg Ala Glu Arg Arg Gly Ser Tyr Pro Phe
211 35 40 45
214 Ile Asp Phe Arg Leu Leu Asn Ser Thr Thr Tyr Ser Gly Glu Ile Gly
215 50 55 60
218 Thr Lys Lys Lys Val Lys Arg Leu Leu Ser Phe Gln Arg Tyr Phe His
219 65 70 75 80
222 Ala Ser Arg Leu Leu Arg Gly Ile Ile Pro Gln Ala Pro Leu His Leu
223 85 90 95
226 Leu Asp Glu Asp Tyr Leu Gly Gln Ala Arg His Met Leu Ser Lys Val
227 100 105 110
230 Gly Met Trp Asp Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly
231 115 120 125
234 Asn Ser Leu Val Thr Leu Leu Cys His Leu Phe Asn Thr His Gly Leu
235 130 135 140
238 Ile His His Phe Lys Leu Asp Met Val Thr Leu His Arg Phe Leu Val
239 145 150 155 160
242 Met Val Gln Glu Asp Tyr His Ser Gln Asn Pro Tyr His Asn Ala Val
243 165 170 175
246 His Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr Leu Lys Glu Pro
247 180 185 190
250 Lys Leu Ala Ser Phe Leu Thr Pro Leu Asp Ile Met Leu Gly Leu Leu
251 195 200 205
254 Ala Ala Ala Ala His Asp Val Asp His Pro Gly Val Asn Gln Pro Phe
255 210 215 220
258 Leu Ile Lys Thr Asn His His Leu Ala Asn Leu Tyr Gln Asn Met Ser
259 225 230 235 240
262 Val Leu Glu Asn His His Trp Arg Ser Thr Ile Gly Met Leu Arg Glu
263 245 250 255
266 Ser Arg Leu Leu Ala His Leu Pro Lys Glu Met Thr Gly Thr Trp Asp
267 260 265 270
270 Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly Asn Ser Leu Val

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275 <211> LENGTH: 807
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277 <213> ORGANISM: Human
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282 gccaaatgtg ttgcatgct gggagatata cgactaaggg gtcagacggg ggttcgtgct      120
284 gaacgccgtg gctcctaccc attcattgac ttccgcctac ttaacagtac aacatactca      180
286 ggggagattg gcaccaagaa aaaggtgaaa agactattaa gctttcaaag atacttccat      240
288 gcatcaaggc tgcttcgtgg aattatacca caagcccctc tgcacctgct ggatgaagac      300
290 taccttggac aagcaaggca tatgctctcc aaagtgggaa tgtgggattt tgacattttc      360
292 ttgtttgata gcttgacaaa tggaaacagc ctggtaacac tgttgtgcca cctcttcaat      420
294 acccatggac tcattcacca tttcaagtta gatatggtga ccttacaccg attttttagtc      480
296 atggttcaag aagattacca cagccaaaac ccgtatcaca atgctgttca cgcagccgac      540
298 gtcacccagg ccatgcactg ctacctgaaa gagccaaagc ttgccagctt cctcacgcct      600
300 ctggacatca tgcttggaat gctggctgca gcagcacacg atgtggacca cccaggggtg      660
302 aaccagccat ttttgataaa aactaaccac catcttgcaa acctatatca gaatatgtct      720
304 gtgctggaga atcatcactg gcgatctaca attggcatgc ttcgagaatc aaggcttctt      780
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310 <211> LENGTH: 450
311 <212> TYPE: PRT
312 <213> ORGANISM: Human
314 <400> SEQUENCE: 5
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321      20      25      30
324 Arg Gly Gln Thr Gly Val Arg Ala Glu Arg Arg Gly Ser Tyr Pro Phe
325      35      40      45
328 Ile Asp Phe Arg Leu Leu Asn Ser Thr Thr Tyr Ser Gly Glu Ile Gly
329      50      55      60
332 Thr Lys Lys Lys Val Lys Arg Leu Leu Ser Phe Gln Arg Tyr Phe His
333 65      70      75      80
336 Ala Ser Arg Leu Leu Arg Gly Ile Ile Pro Gln Ala Pro Leu His Leu
337      85      90      95
340 Leu Asp Glu Asp Tyr Leu Gly Gln Ala Arg His Met Leu Ser Lys Val
341      100      105      110
344 Gly Met Trp Asp Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly
345      115      120      125
348 Asn Ser Leu Val Thr Leu Leu Cys His Leu Phe Asn Thr His Gly Leu
349      130      135      140
352 Ile His His Phe Lys Leu Asp Met Val Thr Leu His Arg Phe Leu Val
353 145      150      155      160
356 Met Val Gln Glu Asp Tyr His Ser Gln Asn Pro Tyr His Asn Ala Val
357      165      170      175
360 His Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr Leu Lys Glu Pro
361      180      185      190

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364 Lys Leu Ala Ser Phe Leu Thr Pro Leu Asp Ile Met Leu Gly Leu Leu
365      195      200      205
368 Ala Ala Ala Ala His Asp Val Asp His Pro Gly Val Asn Gln Pro Phe
369      210      215      220
372 Leu Ile Lys Thr Asn His His Leu Ala Asn Leu Tyr Gln Asn Met Ser
373 225      230      235      240
376 Val Leu Glu Asn His His Trp Arg Ser Thr Ile Gly Met Leu Arg Glu
377      245      250      255
380 Ser Arg Leu Leu Ala His Leu Pro Lys Glu Met Thr Gln Asp Ile Glu
381      260      265      270
384 Gln Gln Leu Gly Ser Leu Ile Leu Ala Thr Asp Ile Asn Arg Gln Asn
385      275      280      285
388 Glu Phe Leu Thr Arg Leu Lys Ala His Leu His Asn Lys Asp Leu Arg
389      290      295      300
392 Leu Glu Asp Ala Gln Asp Arg His Phe Met Leu Gln Ile Ala Leu Lys
393 305      310      315      320
396 Cys Ala Asp Ile Cys Asn Pro Cys Arg Ile Trp Glu Met Ser Lys Gln
397      325      330      335
400 Trp Ser Glu Arg Val Cys Glu Glu Phe Tyr Arg Gln Gly Glu Leu Glu
401      340      345      350
404 Gln Lys Phe Glu Leu Glu Ile Ser Pro Leu Cys Asn Gln Gln Lys Asp
405      355      360      365
408 Ser Ile Pro Ser Ile Gln Ile Gly Phe Met Ser Tyr Ile Val Glu Pro
409      370      375      380
412 Leu Phe Arg Glu Trp Ala His Phe Thr Gly Asn Ser Thr Leu Ser Glu
413 385      390      395      400
416 Asn Met Leu Gly His Leu Ala His Asn Lys Ala Gln Trp Lys Ser Leu
417      405      410      415
420 Leu Pro Arg Gln His Arg Ser Arg Gly Ser Ser Gly Ser Gly Pro Asp
421      420      425      430
424 His Asp His Ala Gly Gln Gly Thr Glu Ser Glu Glu Gln Glu Gly Asp
425      435      440      445
428 Ser Pro
429      450
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433 <211> LENGTH: 1353
434 <212> TYPE: DNA
435 <213> ORGANISM: Human
437 <400> SEQUENCE: 6
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442 gaacgccgtg gctcctaccc attcattgac ttccgcctac ttaacagtac aacatactca      180
444 ggggagattg gcaccaagaa aaagtgaaa agactattaa gctttcaaag atacttccat      240
446 gcatcaaggc tgcttcgttg aattatacca caagcccctc tgcacctgct ggatgaagac      300
448 taccttggac aagcaaggca tatgctctcc aaagtgggaa tgtgggattt tgacatttcc      360
450 ttgtttgatc gcttgacaaa tggaaacagc ctggttaacac tgttgtgcca cctcttcaat      420
452 acccatggac tcattcacca tttcaagtta gatatggtga ccttacaccg atttttagtc      480
454 atggttcaag aagattacca cagccaaaac ccgtatcaca atgctgttca cgcagccgac      540
456 gtcacccagg ccatgcactg ctacctgaaa gagccaaagc ttgccagctt cctcacgcct      600

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VERIFICATION SUMMARY

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